

SEQUENCE LISTING

<110> Yamanouchi Pharmaceutical Co., Ltd.

<120> Canine CYP1A2 genetic polymorphism

<130> Y0414PCT-712

<150> JP 2003-152917

<151> 2003-05-29

<150> JP 2003-206581

<151> 2003-08-07

<160> 23

<170> PatentIn version 3.1

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<212> DNA

<213> Canis familiaris

<220>

<223> Inventor: Tenmizu, Daisuke; Fukunaga, Yasuhisa; Noguchi, Kiyoshi

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 <213> Artificial Sequence

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 GeneRacer RNA Oligo

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 Met Ala Leu Ser Gln Met Ala Thr Glu Leu Leu Leu Ala Ser Thr
 1 5 10 15

atc ttc tgc ttg gta ctc tgg gtg gtc aag gcc tgg cag cct cgg ctt 155
 Ile Phe Cys Leu Val Leu Trp Val Val Lys Ala Trp Gln Pro Arg Leu
 20 25 30

ccc aaa ggc ctg aag agt cca ccg ggg ccc tgg ggc tgg ccc ctg ctc 203
 Pro Lys Gly Leu Lys Ser Pro Pro Gly Pro Trp Gly Trp Pro Leu Leu
 35 40 45

ggg aac gtg ctg acc ttg ggc aag agc ccc cac ctg gcg ctg tcc agg Gly Asn Val Leu Thr Leu Gly Lys Ser Pro His Leu Ala Leu Ser Arg 50 55 60	251
ctg agc cag cgt tat ggg gac gtg ctg cag atc cgc atc ggc tcc acc Leu Ser Gln Arg Tyr Gly Asp Val Leu Gln Ile Arg Ile Gly Ser Thr 65 70 75	299
ccc gtg ctg gtg ctc agt ggc ctg gac acc atc cgg cag gcc ctg gtg Pro Val Leu Val Leu Ser Gly Leu Asp Thr Ile Arg Gln Ala Leu Val 80 85 90 95	347
cgc cag ggg gat gat ttc aag ggc cgg ccc gac ctc tac agc ttc tct Arg Gln Gly Asp Asp Phe Lys Gly Arg Pro Asp Leu Tyr Ser Phe Ser 100 105 110	395
ctg gtg acc gac ggc caa agc ctg acc ttc agc cca gac tcc gga cca Leu Val Thr Asp Gly Gln Ser Leu Thr Phe Ser Pro Asp Ser Gly Pro 115 120 125	443
gtg tgg gct gcg cgc agg cgc ctg gct cag aac gcg ctc aac acc ttc Val Trp Ala Ala Arg Arg Arg Leu Ala Gln Asn Ala Leu Asn Thr Phe 130 135 140	491
tcc att gcc tcc gac cgg gct tcc tcg tgc tct tgc tac ctg gaa gag Ser Ile Ala Ser Asp Pro Ala Ser Ser Cys Ser Cys Tyr Leu Glu Glu 145 150 155	539
cat gtg agc aag gag gcc gag gcc ctt ctc agc agg ctg cag gag cag His Val Ser Lys Glu Ala Glu Ala Leu Leu Ser Arg Leu Gln Glu Gln 160 165 170 175	587
atg gca gag gtt ggg cgc ttt gat ccc tac aac caa gtg ctg atg tca Met Ala Glu Val Gly Arg Phe Asp Pro Tyr Asn Gln Val Leu Met Ser 180 185 190	635
gtg gcc aat gtc att ggt gca atg tgc ttt ggg cac cac ttc tct cag Val Ala Asn Val Ile Gly Ala Met Cys Phe Gly His His Phe Ser Gln 195 200 205	683
aga agt gag gaa atg ctc ccc ctc cta atg agc tcc agt gat ttt gtg Arg Ser Glu Glu Met Leu Pro Leu Leu Met Ser Ser Ser Asp Phe Val 210 215 220	731
gag acc gtc tcc aac ggg aac cgg gtg gac ttt ttc ccc att ctc caa Glu Thr Val Ser Asn Gly Asn Pro Val Asp Phe Phe Pro Ile Leu Gln 225 230 235	779

tat atg ccc aac tca gcc ctg cag aga ttc aag aac ttc aac cag acg Tyr Met Pro Asn Ser Ala Leu Gln Arg Phe Lys Asn Phe Asn Gln Thr 240 245 250 255	827
ttc gtg cag tcc ctg cag aaa att gtc cag gaa cac tat caa gac ttt Phe Val Gln Ser Leu Gln Lys Ile Val Gln Glu His Tyr Gln Asp Phe 260 265 270	875
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gag aag agc tcc agg gct agt gat ggc cac atc ccc caa gag aag att Glu Lys Ser Ser Arg Ala Ser Asp Gly His Ile Pro Gln Glu Lys Ile 290 295 300	971
gtc aac ctt atc aac gac att ttt ggg gcc gga ttt gac act gtc aca Val Asn Leu Ile Asn Asp Ile Phe Gly Ala Gly Phe Asp Thr Val Thr 305 310 315	1019
acg gcc att tcc tgg agt ctt atg tac ctt gtg gca aac cct gag ata Thr Ala Ile Ser Trp Ser Leu Met Tyr Leu Val Ala Asn Pro Glu Ile 320 325 330 335	1067
cag aga aag atc cag aag gag ttg gac acg gtg att ggc agg gca cgg Gln Arg Lys Ile Gln Lys Glu Leu Asp Thr Val Ile Gly Arg Ala Arg 340 345 350	1115
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gaa tgc tgt gtc ttc ata aac cag tgg cag gtc aat cat gac caa sag Glu Cys Cys Val Phe Ile Asn Gln Trp Gln Val Asn His Asp Gln Xaa 400 405 410 415	1307
gtg tgg ggg gat cca ttt gca ttc cgg cca gag cga ttc ctc act gca Val Trp Gly Asp Pro Phe Ala Phe Arg Pro Glu Arg Phe Leu Thr Ala 420 425 430	1355

gat ggy acc rcc atc aac aag acc ttg agt gag aag gtg atg ctc ttt 1403
 Asp Xaa Thr Xaa Ile Asn Lys Thr Leu Ser Glu Lys Val Met Leu Phe
 435 440 445

 ggc atg ggc aag cgc cgg tgc ata gga gag gtc ctg gcc aag tgg gag 1451
 Gly Met Gly Lys Arg Arg Cys Ile Gly Glu Val Leu Ala Lys Trp Glu
 450 455 460

 atc ttc ctc ttc cta gcc atc ttg ctg cag cgg ctg gag ttc agc gtg 1499
 Ile Phe Leu Phe Leu Ala Ile Leu Leu Gln Arg Leu Glu Phe Ser Val
 465 470 475

 cca gca ggt gtg aaa gta gac cta acc ccc atc tat ggg ctg acc atg 1547
 Pro Ala Gly Val Lys Val Asp Leu Thr Pro Ile Tyr Gly Leu Thr Met
 480 485 490 495

 aag cac acc cgc tgt gag cat gtc cag gca cgg cca cgc ttc tcc atc 1595
 Lys His Thr Arg Cys Glu His Val Gln Ala Arg Pro Arg Phe Ser Ile
 500 505 510

 aag tga aggcaccagc atgycaaggc agagggagga gaaggat 1638
 Lys

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 <222> (435)..(435)
 <223> The 'Xaa' at location 435 stands for Ala or Thr.

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Lys Gly Leu Lys Ser Pro Pro Gly Pro Trp Gly Trp Pro Leu Leu Gly
35 40 45

Asn Val Leu Thr Leu Gly Lys Ser Pro His Leu Ala Leu Ser Arg Leu
50 55 60

Ser Gln Arg Tyr Gly Asp Val Leu Gln Ile Arg Ile Gly Ser Thr Pro
65 70 75 80

Val Leu Val Leu Ser Gly Leu Asp Thr Ile Arg Gln Ala Leu Val Arg
85 90 95

Gln Gly Asp Asp Phe Lys Gly Arg Pro Asp Leu Tyr Ser Phe Ser Leu
100 105 110

Val Thr Asp Gly Gln Ser Leu Thr Phe Ser Pro Asp Ser Gly Pro Val
115 120 125

Trp Ala Ala Arg Arg Arg Leu Ala Gln Asn Ala Leu Asn Thr Phe Ser
130 135 140

Ile Ala Ser Asp Pro Ala Ser Ser Cys Ser Cys Tyr Leu Glu Glu His
145 150 155 160

Val Ser Lys Glu Ala Glu Ala Leu Leu Ser Arg Leu Gln Glu Gln Met
165 170 175

Ala Glu Val Gly Arg Phe Asp Pro Tyr Asn Gln Val Leu Met Ser Val
180 185 190

Ala Asn Val Ile Gly Ala Met Cys Phe Gly His His Phe Ser Gln Arg
 195 200 205

Ser Glu Glu Met Leu Pro Leu Leu Met Ser Ser Ser Asp Phe Val Glu
 210 215 220

Thr Val Ser Asn Gly Asn Pro Val Asp Phe Phe Pro Ile Leu Gln Tyr
 225 230 235 240

Met Pro Asn Ser Ala Leu Gln Arg Phe Lys Asn Phe Asn Gln Thr Phe
 245 250 255

Val Gln Ser Leu Gln Lys Ile Val Gln Glu His Tyr Gln Asp Phe Asp
 260 265 270

Glu Arg Ser Val Gln Asp Ile Thr Gly Ala Leu Leu Lys His Asn Glu
 275 280 285

Lys Ser Ser Arg Ala Ser Asp Gly His Ile Pro Gln Glu Lys Ile Val
 290 295 300

Asn Leu Ile Asn Asp Ile Phe Gly Ala Gly Phe Asp Thr Val Thr Thr
 305 310 315 320

Ala Ile Ser Trp Ser Leu Met Tyr Leu Val Ala Asn Pro Glu Ile Gln
 325 330 335

Arg Lys Ile Gln Lys Glu Leu Asp Thr Val Ile Gly Arg Ala Arg Gln
 340 345 350

Pro Arg Leu Ser Asp Arg Pro Gln Leu Pro Leu Met Glu Ala Phe Ile
 355 360 365

Leu Glu Ile Phe Arg His Thr Ser Phe Val Pro Phe Thr Ile Pro His
 370 375 380

Ser Thr Thr Lys Asp Thr Thr Leu Lys Gly Phe Tyr Ile Pro Lys Glu
 385 390 395 400

Cys Cys Val Phe Ile Asn Gln Trp Gln Val Asn His Asp Gln Xaa Val
 405 410 415

Trp Gly Asp Pro Phe Ala Phe Arg Pro Glu Arg Phe Leu Thr Ala Asp
 420 425 430

Xaa Thr Xaa Ile Asn Lys Thr Leu Ser Glu Lys Val Met Leu Phe Gly
 435 440 445

Met Gly Lys Arg Arg Cys Ile Gly Glu Val Leu Ala Lys Trp Glu Ile
 450 455 460

Phe Leu Phe Leu Ala Ile Leu Leu Gln Arg Leu Glu Phe Ser Val Pro
 465 470 475 480

Ala Gly Val Lys Val Asp Leu Thr Pro Ile Tyr Gly Leu Thr Met Lys
 485 490 495

His Thr Arg Cys Glu His Val Gln Ala Arg Pro Arg Phe Ser Ile Lys
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